



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source

Date Processed by STIC:

10/800,024  
IFW0  
3/28/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313 1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/800,024

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
                    scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                    is Artificial Sequence
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                    "Unknown." Please explain source of genetic material in <220> to <223> section.  
                    (See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
                    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                    listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 03/22/2004

PATENT APPLICATION: US/10/800,024

TIME: 09:31:57

Input Set : A:\SYR-HSD-5001-C1.ST25.txt

Output Set: N:\CRF4\03222004\J800024.raw

1

3 <110> APPLICANT: Syrrx, Inc.

5 <120> TITLE OF INVENTION: CRYSTALLIZATION OF 11-BETA-HYDROXYSTEROID DEHYDROGENASE TYPE

7 <130> FILE REFERENCE: SYR-HSD-5001-C1

C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/800,024

10 <141> CURRENT FILING DATE: 2004-03-12

12 <160> NUMBER OF SEQ ID NOS: 13

14 <170> SOFTWARE: PatentIn version 3.2

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 292

18 <212> TYPE: PRT

19 <213> ORGANISM: Homo sapiens

22 <220> FEATURE:

W--> 23 <221> NAME/KEY: Amino acid sequence for full-length human wild type

W--> 24 11-beta-hydroxysteroid dehydrogenase type 1

25 <222> LOCATION: (1)..(292)

27 <400> SEQUENCE: 1

29	Met	Ala	Phe	Met	Lys	Lys	Tyr	Leu	Leu	Pro	Ile	Leu	Gly	Leu	Phe	Met
30	1				5					10					15	
33	Ala	Tyr	Tyr	Tyr	Tyr	Ser	Ala	Asn	Glu	Glu	Phe	Arg	Pro	Glu	Met	Leu
34					20				25					30		
37	Gln	Gly	Lys	Lys	Val	Ile	Val	Thr	Gly	Ala	Ser	Lys	Gly	Ile	Gly	Arg
38			35					40					45			
41	Glu	Met	Ala	Tyr	His	Leu	Ala	Lys	Met	Gly	Ala	His	Val	Val	Val	Thr
42		50					55					60				
45	Ala	Arg	Ser	Lys	Glu	Thr	Leu	Gln	Lys	Val	Val	Ser	His	Cys	Leu	Glu
46	65				70				75					80		
49	Leu	Gly	Ala	Ala	Ser	Ala	His	Tyr	Ile	Ala	Gly	Thr	Met	Glu	Asp	Met
50				85				90					95			
53	Thr	Phe	Ala	Glu	Gln	Phe	Val	Ala	Gln	Ala	Gly	Lys	Leu	Met	Gly	Gly
54			100					105					110			
57	Leu	Asp	Met	Leu	Ile	Leu	Asn	His	Ile	Thr	Asn	Thr	Ser	Leu	Asn	Leu
58		115					120						125			
61	Phe	His	Asp	Asp	Ile	His	His	Val	Arg	Lys	Ser	Met	Glu	Val	Asn	Phe
62		130					135					140				
65	Leu	Ser	Tyr	Val	Val	Leu	Thr	Val	Ala	Ala	Leu	Pro	Met	Leu	Lys	Gln
66	145				150				155				160			
69	Ser	Asn	Gly	Ser	Ile	Val	Val	Val	Ser	Ser	Leu	Ala	Gly	Lys	Val	Ala
70				165				170					175			
73	Tyr	Pro	Met	Val	Ala	Ala	Tyr	Ser	Ala	Ser	Lys	Phe	Ala	Leu	Asp	Gly
74			180					185					190			
77	Phe	Phe	Ser	Ser	Ile	Arg	Lys	Glu	Tyr	Ser	Val	Ser	Arg	Val	Asn	Val
78			195				200						205			
81	Ser	Ile	Thr	Leu	Cys	Val	Leu	Gly	Leu	Ile	Asp	Thr	Glu	Thr	Ala	Met

Does Not Comply  
Corrected Diskette Needed  
(P3.1-6)

From  
delete, 221  
and insert  
this response  
into section  
223.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/800,024

DATE: 03/22/2004

TIME: 09:31:57

Input Set : A:\SYR-HSD-5001-C1.ST25.txt

Output Set: N:\CRF4\03222004\J800024.raw

```

82      210      215      220
85 Lys Ala Val Ser Gly Ile Val His Met Gln Ala Ala Pro Lys Glu Glu
86 225      230      235      240
89 Cys Ala Leu Glu Ile Ile Lys Gly Gly Ala Leu Arg Gln Glu Glu Val
90      245      250      255
93 Tyr Tyr Asp Ser Ser Leu Trp Thr Thr Leu Leu Ile Arg Asn Pro Cys
94      260      265      270
97 Arg Lys Ile Leu Glu Phe Leu Tyr Ser Thr Ser Tyr Asn Met Asp Arg
98      275      280      285
101 Phe Ile Asn Lys
102      290
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 807
107 <212> TYPE: DNA
108 <213> ORGANISM: Homo sapiens
111 <220> FEATURE:
W--> 112 <221> NAME/KEY: Human cDNA sequence encoding residues 24-292 of
W--> 113 11-beta-hydroxysteroid dehydrogenase type 1
114 <222> LOCATION: (1)..(807)
116 <400> SEQUENCE: 2
117 aacgaggaat tcagaccaga gatgctccaa ggaaagaaag tgattgtcac aggggccagc      60
119 aaaggggatcg gaagagagat ggcttatcat ctggcgaaaga tgggagccca tgtggtggtg      120
121 acagcgaggt caaaagaaac tctacagaag gtggtatccc actgcctgga gcttggagca      180
123 gcttcagcac actacattgc tggcaccatg gaagacatga ccttcgcaga gcaatttggt      240
125 gcccaagcag gaaagctcat gggaggacta gacatgctca ttctcaacca catcaccaac      300
127 acttctttga atctttttca tgatgatatt caccatgtgc gcaaaagcat ggaagtcaac      360
129 ttcttcagtt acgtggctct gactgtagct gccttgccca tgctgaagca gagcaatgga      420
131 agcattgttg tctctctctc tctggctggg aaagtggctt atccaatggt tgctgcctat      480
133 tctgcaagca agtttgcttt ggatgggttc ttctctcca tcagaaagga atattcagtg      540
135 tccagggtea atgtatcaat cactctctgt gttcttggcc tcatagacac agaaacagcc      600
137 atgaaggcag tttctgggat agtccatatg caagcagctc caaaggagga atgtgccttg      660
139 gagatcatca aagggggagc tctgcgccaa gaagaagtgt attatgacag ctcaactctg      720
141 accactcttc tgatcagaaa tccatgcagg aagatcctgg aatttctcta ctcaacgagc      780
143 tataatatgg acagattcat aaacaag
146 <210> SEQ ID NO: 3
147 <211> LENGTH: 705
148 <212> TYPE: DNA
149 <213> ORGANISM: Homo sapiens
152 <220> FEATURE:
W--> 153 <221> NAME/KEY: Human cDNA sequence encoding residues 24-258 of
W--> 154 11-beta-hydroxysteroid dehydrogenase type 1
155 <222> LOCATION: (1)..(705)
157 <400> SEQUENCE: 3
158 aacgaggaat tcagaccaga gatgctccaa ggaaagaaag tgattgtcac aggggccagc      60
160 aaaggggatcg gaagagagat ggcttatcat ctggcgaaaga tgggagccca tgtggtggtg      120
162 acagcgaggt caaaagaaac tctacagaag gtggtatccc actgcctgga gcttggagca      180
164 gcttcagcac actacattgc tggcaccatg gaagacatga ccttcgcaga gcaatttggt      240
166 gcccaagcag gaaagctcat gggaggacta gacatgctca ttctcaacca catcaccaac      300
168 acttctttga atctttttca tgatgatatt caccatgtgc gcaaaagcat ggaagtcaac      360

```

move to  
(2237)

move to  
(2237)

## RAW SEQUENCE LISTING

DATE: 03/22/2004

PATENT APPLICATION: US/10/800,024

TIME: 09:31:57

Input Set : A:\SYR-HSD-5001-C1.ST25.txt

Output Set: N:\CRF4\03222004\J800024.raw

170 ttccctcagtt acgtgggtcct gactgtagct gccttgccca tgctgaagca gagcaatgga 420  
 172 agcattgttg tcgtctctctc tctggctggg aaagtggctt atccaatggt tgctgcctat 480  
 174 tctgcaagca agtttgcttt ggatgggttc ttctctcca tcagaaagga atattcagt 540  
 176 tccaggggtca atgtatcaat cactctctgt gttcttggtc tcatagacac agaaacagcc 600  
 178 atgaaggcag tttctgggat agtccatatg caagcagctc caaaggagga atgtgcctg 660  
 180 gagatcatca aagggggagc tctgcgcca gaagaagtgt attat 705  
 183 <210> SEQ ID NO: 4  
 184 <211> LENGTH: 732  
 185 <212> TYPE: DNA  
 186 <213> ORGANISM: Homo sapiens  
 189 <220> FEATURE:  
 W--> 190 <221> NAME/KEY: Human cDNA sequence encoding residues 24-267 of  
 W--> 191 11-beta-hydroxysteroid dehydrogenase type 1

move to  
223

192 <222> LOCATION: (1)..(732)  
 194 <400> SEQUENCE: 4  
 195 aacgaggaat tcagaccaga gatgctccaa ggaaagaaag tgattgtcac aggggccagc 60  
 197 aaaggggatcg gaagagagat ggcttatcat ctggcgaaag tgggagccca tgtggtggtg 120  
 199 acagcgaggt caaaagaaac tctacagaag gtggtatccc actgcttga gcttggagca 180  
 201 gcctcagcac actacattgc tggcaccatg gaagacatga ccttcgcaga gcaatttgtt 240  
 203 gcccaagcag gaaagctcat gggaggacta gacatgtca ttctcaacca catcaccaac 300  
 205 acttctttga atctttttca tgatgatatt caccatgtgc gcaaaagcat ggaagtcaac 360  
 207 ttctcagtt acgtgggtcct gactgtagct gccttgccca tgctgaagca gagcaatgga 420  
 209 agcattgttg tcgtctctctc tctggctggg aaagtggctt atccaatggt tgctgcctat 480  
 211 tctgcaagca agtttgcttt ggatgggttc ttctctcca tcagaaagga atattcagt 540  
 213 tccaggggtca atgtatcaat cactctctgt gttcttggtc tcatagacac agaaacagcc 600  
 215 atgaaggcag tttctgggat agtccatatg caagcagctc caaaggagga atgtgcctg 660  
 217 gagatcatca aagggggagc tctgcgcca gaagaagtgt attatgacag ctactctgg 720  
 219 accactcttc tg 732  
 222 <210> SEQ ID NO: 5  
 223 <211> LENGTH: 286  
 224 <212> TYPE: PRT  
 225 <213> ORGANISM: Custom  
 228 <220> FEATURE:

W--> 229 <221> NAME/KEY: Amino acid sequence for residues 24-292 of 11-beta-hydroxysteroid  
 W--> 230 dehydrogenase type 1 with a N-terminal MKHQHQHQHQHQHQOPL tag

231 <222> LOCATION: (1)..(286)  
 233 <400> SEQUENCE: 5  
 235 Met Lys His Gln His Gln His Gln His Gln Gln Pro  
 236 1 5 10 15  
 239 Leu Asn Glu Glu Phe Arg Pro Glu Met Leu Gln Gly Lys Lys Val Ile  
 240 20 25 30  
 243 Val Thr Gly Ala Ser Lys Gly Ile Gly Arg Glu Met Ala Tyr His Leu  
 244 35 40 45  
 247 Ala Lys Met Gly Ala His Val Val Val Thr Ala Arg Ser Lys Glu Thr  
 248 50 55 60  
 251 Leu Gln Lys Val Val Ser His Cys Leu Glu Leu Gly Ala Ala Ser Ala  
 252 65 70 75 80  
 255 His Tyr Ile Ala Gly Thr Met Glu Asp Met Thr Phe Ala Glu Gln Phe  
 256 85 90 95

INVALID (213)  
 Response, see item # 10  
 move to (223)

on error  
summary  
sheet

## RAW SEQUENCE LISTING

DATE: 03/22/2004

PATENT APPLICATION: US/10/800,024

TIME: 09:31:57

Input Set : A:\SYR-HSD-5001-C1.ST25.txt

Output Set: N:\CRF4\03222004\J800024.raw

259 Val Ala Gln Ala Gly Lys Leu Met Gly Gly Leu Asp Met Leu Ile Leu  
 260 100 105 110  
 263 Asn His Ile Thr Asn Thr Ser Leu Asn Leu Phe His Asp Asp Ile His  
 264 115 120 125  
 267 His Val Arg Lys Ser Met Glu Val Asn Phe Leu Ser Tyr Val Val Leu  
 268 130 135 140  
 271 Thr Val Ala Ala Leu Pro Met Leu Lys Gln Ser Asn Gly Ser Ile Val  
 272 145 150 155 160  
 275 Val Val Ser Ser Leu Ala Gly Lys Val Ala Tyr Pro Met Val Ala Ala  
 276 165 170 175  
 279 Tyr Ser Ala Ser Lys Phe Ala Leu Asp Gly Phe Phe Ser Ser Ile Arg  
 280 180 185 190  
 283 Lys Glu Tyr Ser Val Ser Arg Val Asn Val Ser Ile Thr Leu Cys Val  
 284 195 200 205  
 287 Leu Gly Leu Ile Asp Thr Glu Thr Ala Met Lys Ala Val Ser Gly Ile  
 288 210 215 220  
 291 Val His Met Gln Ala Ala Pro Lys Glu Glu Cys Ala Leu Glu Ile Ile  
 292 225 230 235 240  
 295 Lys Gly Gly Ala Leu Arg Gln Glu Glu Val Tyr Tyr Asp Ser Ser Leu  
 296 245 250 255  
 299 Trp Thr Thr Leu Ile Arg Asn Pro Cys Arg Lys Ile Leu Glu Phe  
 300 260 265 270  
 303 Leu Tyr Ser Thr Ser Tyr Asn Met Asp Arg Phe Ile Asn Lys  
 304 275 280 285  
 307 <210> SEQ ID NO: 6  
 308 <211> LENGTH: 252  
 309 <212> TYPE: PRT  
 310 <213> ORGANISM: Custom  
 313 <220> FEATURE:  
 W--> 314 <221> NAME/KEY: Amino acid sequence for residues 24-258 of 11-beta-hydroxysteroid  
 W--> 315 dehydrogenase type 1 with a N-terminal MKHQHQHQHQHQOQPL tag  
 316 <222> LOCATION: (1)..(252)  
 318 <400> SEQUENCE: 6  
 320 Met Lys His Gln His Gln His Gln His Gln His Gln Gln Pro  
 321 1 5 10 15  
 324 Leu Asn Glu Glu Phe Arg Pro Glu Met Leu Gln Gly Lys Lys Val Ile  
 325 20 25 30  
 328 Val Thr Gly Ala Ser Lys Gly Ile Gly Arg Glu Met Ala Tyr His Leu  
 329 35 40 45  
 332 Ala Lys Met Gly Ala His Val Val Val Thr Ala Arg Ser Lys Glu Thr  
 333 50 55 60  
 336 Leu Gln Lys Val Val Ser His Cys Leu Glu Leu Gly Ala Ala Ser Ala  
 337 65 70 75 80  
 340 His Tyr Ile Ala Gly Thr Met Glu Asp Met Thr Phe Ala Glu Gln Phe  
 341 85 90 95  
 344 Val Ala Gln Ala Gly Lys Leu Met Gly Gly Leu Asp Met Leu Ile Leu  
 345 100 105 110  
 348 Asn His Ile Thr Asn Thr Ser Leu Asn Leu Phe His Asp Asp Ile His  
 349 115 120 125

INVALID  
 (2137) Response, see item # 10 on  
 error summary sheet.

move  
 to (223)

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/800,024

DATE: 03/22/2004

TIME: 09:31:57

Input Set : A:\SYR-HSD-5001-C1.ST25.txt

Output Set: N:\CRF4\03222004\J800024.raw

```

352 His Val Arg Lys Ser Met Glu Val Asn Phe Leu Ser Tyr Val Val Leu
353      130      135      140
356 Thr Val Ala Ala Leu Pro Met Leu Lys Gln Ser Asn Gly Ser Ile Val
357 145      150      155      160
360 Val Val Ser Ser Leu Ala Gly Lys Val Ala Tyr Pro Met Val Ala Ala
361      165      170      175
364 Tyr Ser Ala Ser Lys Phe Ala Leu Asp Gly Phe Phe Ser Ser Ile Arg
365      180      185      190
368 Lys Glu Tyr Ser Val Ser Arg Val Asn Val Ser Ile Thr Leu Cys Val
369      195      200      205
372 Leu Gly Leu Ile Asp Thr Glu Thr Ala Met Lys Ala Val Ser Gly Ile
373      210      215      220
376 Val His Met Gln Ala Ala Pro Lys Glu Glu Cys Ala Leu Glu Ile Ile
377 225      230      235      240
380 Lys Gly Gly Ala Leu Arg Gln Glu Glu Val Tyr Tyr
381      245      250

```

384 &lt;210&gt; SEQ ID NO: 7

385 &lt;211&gt; LENGTH: 261

386 &lt;212&gt; TYPE: PRT

387 &lt;213&gt; ORGANISM: Custom

390 &lt;220&gt; FEATURE:

W--> 391 <221> NAME/KEY: Amino acid sequence for residues 24-267 of 11-beta-hydroxysteroid  
W--> 392 dehydrogenase type 1 with a N-terminal MKHQHQHQHQHQHQPL tag

393 &lt;222&gt; LOCATION: (1)..(261)

395 &lt;400&gt; SEQUENCE: 7

```

397 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Gln Pro
398 1      5      10      15
401 Leu Asn Glu Glu Phe Arg Pro Glu Met Leu Gln Gly Lys Lys Val Ile
402      20      25      30
405 Val Thr Gly Ala Ser Lys Gly Ile Gly Arg Glu Met Ala Tyr His Leu
406      35      40      45
409 Ala Lys Met Gly Ala His Val Val Val Thr Ala Arg Ser Lys Glu Thr
410      50      55      60
413 Leu Gln Lys Val Val Ser His Cys Leu Glu Leu Gly Ala Ala Ser Ala
414 65      70      75      80
417 His Tyr Ile Ala Gly Thr Met Glu Asp Met Thr Phe Ala Glu Gln Phe
418      85      90      95
421 Val Ala Gln Ala Gly Lys Leu Met Gly Gly Leu Asp Met Leu Ile Leu
422      100     105     110
425 Asn His Ile Thr Asn Thr Ser Leu Asn Leu Phe His Asp Asp Ile His
426      115     120     125
429 His Val Arg Lys Ser Met Glu Val Asn Phe Leu Ser Tyr Val Val Leu
430      130     135     140
433 Thr Val Ala Ala Leu Pro Met Leu Lys Gln Ser Asn Gly Ser Ile Val
434 145     150     155     160
437 Val Val Ser Ser Leu Ala Gly Lys Val Ala Tyr Pro Met Val Ala Ala
438      165     170     175
441 Tyr Ser Ala Ser Lys Phe Ala Leu Asp Gly Phe Phe Ser Ser Ile Arg
442      180     185     190

```

same errors

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

## VERIFICATION SUMMARY

DATE: 03/22/2004

PATENT APPLICATION: US/10/800,024

TIME: 09:31:58

Input Set : A:\SYR-HSD-5001-C1.ST25.txt

Output Set: N:\CRF4\03222004\J800024.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:23 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:24 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:1 ✓  
L:112 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:113 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:2 ✓  
L:153 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:154 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:3 ✓  
L:190 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:191 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:4 ✓  
L:229 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:230 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:5 ✓  
L:314 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:315 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:6 ✓  
L:391 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7 ✓  
L:392 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:7 ✓  
L:472 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:486 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
L:500 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:514 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
L:528 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
L:542 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13